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GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 4, 2002, 07:40:45 ; Search time 37.8 Seconds

(without alignments)  
4205.882 Million cell updates/sec

Title: US-08-153-397a-2  
Perfect score: 4928  
Sequence: 1 MGPEAISLLLVLVAVSGDA.....QRPPFSQLHRLAEDALNTV 919

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL\_19;\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

No. Score Query Length DB ID Description

1 4534 92.0 911 11 035407 ID 035407 PRELIMINARY; PRT; 911 AA.

2 2387 48.4 840 11 099857 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

3 1159 23.5 220 11 064108 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

4 1044 21.2 797 5 0952V6 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

5 1023 20.8 767 5 0952V6 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

6 929 5 18.9 183 11 064107 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

7 691 14.0 700 5 018433 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

8 648 13.1 1145 5 098112 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

9 633 12.8 811 13 09PH43 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

10 633 12.8 821 13 09PH44 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

11 631 12.8 826 13 09PRT9 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

12 628 5 12.8 790 13 090699 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

13 623 5 12.7 699 5 027656 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

14 622 5 12.7 839 4 07562 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

15 615 12.5 503 4 015655 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

16 614 12.5 591 4 015656 ID 035407; AC 035407; DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

17	611	12.4	757	5	Q18163	Q18163 caenorhabdi
18	608	12.3	282	13	Q91373	Q91373 xenopus. tr
19	608	12.3	902	5	Q17576	Q17576 caenorhabdi
20	608	12.3	928	5	Q9B1X1	Q9B1X1 caenorhabdi
21	597.5	12.1	946	13	Q07153	Q07153 torpedo cal
22	593.5	12.0	868	11	Q24488	Q24488 drosophila
23	590	12.0	868	11	Q92899	Q92899 abelision mur
24	590	12.0	871	11	Q61066	Q61066 mus musculu
25	588.5	11.9	869	4	Q17146	Q17146 homo sapien
26	588.5	11.9	881	11	Q61988	Q61988 mus musculu
27	587.5	11.9	860	11	Q51005	Q61005 mus musculu
28	584	11.9	685	5	Q24488	Q24488 drosophila
29	576	11.7	981	15	Q9Y6KX	Q9Y6KX drosophila
30	574	11.6	168	11	Q22209	Q22209 ratetus norv
31	571	11.6	737	5	Q17305	Q17305 caenorhabdi
32	552	11.2	354	13	Q9DDA2	Q9DDA2 xenopus lae
33	548	11.1	989	13	Q9PN66	Q9PN66 gallus galli
34	541.5	12.45	1245	13	Q9YG88	Q9YG88 scophthalmu
35	538.5	10.9	724	5	Q9PV24	Q9PV24 xenopus lae
36	529	10.7	1362	13	Q9PV86	Q9PV86 drosophila
37	523	10.6	1504	5	Q9V86	Q63130 ratetus norv
38	522.5	10.6	2317	11	Q63132	Q63132 ratetus norv
39	522.5	10.6	2338	11	Q63132	Q63132 homo sapien
40	522	10.6	984	4	Q43718	Q43718 homo sapien
41	521	10.6	1358	13	Q73798	Q73798 xenopus lae
42	520	10.6	818	15	Q9PW33	Q9PW33 abelision mur
43	518	10.5	2340	11	Q64736	Q64736 mus musculu
44	515	10.5	1418	13	Q93457	Q93457 scophthalmu
45	512.5	10.4	863	5	Q76148	Q76148 anophelles s



QY	247	LRWPGIDYVGNSNHSTSSGYVEMEFEFDRLRAFOAMQVHCMNHTLGARLPGVGEVCRF	306
Db	243	YHWPGIDYVGNSNHSTSSGYVEMEFEFDRLRAFOAMQVHCMNHTLGARLPGVGEVCRF	301
QY	307	RQPMAMWEGEPMRHNIGGNLDPPIRPARAVSPVPLGGYARFLCFLGPMLSEFIS	366
Db	302	RSEASEWEPTAVSPFLVLDYDNPSPARFVTPQDQRMASAIIQYHEDATWMSEITFOS	361
QY	367	D--WVNNSPALGGTFFPAPWPPGPPPTNSSLERPRGQOPVAKAEGSPPTAIIGLV	424
Db	362	DRAMYNN-----GAITSP-----MAPTYDPMKVDSDNTRILIGCLV	401
QY	425	AIIILILILILALMLWRLHWRLLSKAERRVLEELTVHLSVPGDITLNNR--PGPRE	480
Db	402	AIFIFIAIIVILWQFWQMLKASRMLDDEMVTSLSPSESSMENNVRSSPSEOE	461
QY	481	P-----PYCERPRPGGNPSPASACPVNGSALLSPVARYLATAARPPGP	529
Db	462	SNSTYHRIFPLRPDIQP-----SRLRLKLFEP-----	489
QY	530	PTPARAKPTNQAYASDYMEEPERKGAPLPPPPQNSVPHAEADIVTLOGTGGNTIYAP	589
Db	490	-----AGPEESEGGSSVVKAQPNP-----ECVPHAEADIVNLYGTVGNTYSP	535
QY	590	ALPPGAVGDGPPRV-DFPDRSLRFKFLKGECQFGEVHLCEDVSDPDLDFPLNTRKGH	648
Db	537	AVTMPLISGKDVAAVEEPRPKLTFKEMGEGQFGEVHLCVEGMEKFIDKDFALYVSANQ	596
QY	649	PILVAVKILRDPDKNAESLFSRDFLKEVCKIMSLKDPIITLIGVQVDDPLOMID	708
Db	597	PVLVAVKMLRDAKNA-----RNDFLKEIIMSLKDPIITLIGVQVDDPLOMITE	650
QY	709	YMEGDLNQTSASHOLEDKAEGARGDQQAQGPTISYPMILHVAQIASQMRVYATNF	768
Db	651	YMEGDLNQTSASHOLEDKAEGARGDQQAQGPTISYPMILHVAQIASQMRVYATNF	700
QY	769	VRHDIAATRNCLVGENETIKTADFGMSRNLVAGYYRVQGRAVLPIRWMANECILAGKFT	828
Db	701	VRHDIAATRNCLVGENETIKTADFGMSRNLVAGYYRVQGRAVLPIRWMANECILAGKFT	760
QY	829	ASDWWAFGVILWEVIMLCRAQPEGLTDQEVTEIYAGEFFRDOQGROYLSRPACQGLVE	898
Db	761	AGDWWAFGVILWEVIMLCRAQPEGLTDQEVTEIYAGEFFRDOQGROYLSRPACQGLVE	820
Qy	889	LMRROWSRESEQRPPFSQLH	908
Db	821	LMLSCWRERKHKRSFQEIH	840
RESULT	3		
Q5ZV7			
ID	Q95ZV7	PRELIMINARY;	PRT;
AC	Q95ZV7;		797 AA.
DT	01-DEC-2001	(TREMBLRE. 19, Created)	
DT	01-DEC-2001	(TREMBLRE. 19, Last sequence update)	
DE		HYPOTHETICAL PROTEIN F11D5.3A.	
GN		F11D5.3.	
OS		Caenorhabditis elegans.	
OC		eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Peltoderaiae; Caenorhabditis.	
OX		NCBI-TaxID=6239;	
RN	[1]		
RP		SEQUENCE FROM N.A.	
RC		STRAIN-BRISTOL N2;	
RX		MEDLINE=9969613; PubMed=9851916;	
RA		None;	
RT		"Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium.";	
RL		Science 282:2012-2018(1998).	
RN	[2]		
RP		SEQUENCE FROM N.A.	
RC		STRAIN-BRISTOL N2;	
RA		Nhan M.;	
RT		"The sequence of <i>C. elegans</i> cosmid F11D5.;"	
RL		Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.	
RN	[3]		
RP		SEQUENCE FROM N.A.	
RC		STRAIN-BRISTOL N2;	
RA		Waterson R.;	
RT		"Direct Submission.";	
RL		Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.	
DR		EMBL: U41532; AAC68319.1; -;	
SO		SEQUENCE 797 AA; 90302 MW; C96016AEE144899E CRC64;	
Query Match	21.2%	Score 1044; DB 5; Length 797;	
Best Local Similarity	29.2%	Pred. No. 1.6e74; Mismatches 323; Indels 184; Gaps 31;	
Matches	273;	Conservative 155; Mismatches 323; Indels 184; Gaps 31;	
RA	9	LILJLIVASODADMKGHDFPKCKALGMDRTPSDISSASSWS-DSTAARKRSLESS	67
RT		SGGAWCPACSVFKEEYVQDQLHLVALVSTQGRHAGGLKEFSSRSYRLYRSQG-126	
RL	3	LILYFGVTFHSNTVALERECCHOLGNSKRDQFQASSFDLQGPHARHQE	62
DR	68	DGDGAWCPACSVFKEEYVQDQLHLVALVSTQGRHAGGLKEFSSRSYRLYRSQG-126	
KW	63	SGGAWCPACSVFKEEYVQDQLHLVALVSTQGRHAGGLKEFSSRSYRLYRSQG-122	
SEQUENCE	1	SGGAWCPACSVFKEEYVQDQLHLVALVSTQGRHAGGLKEFSSRSYRLYRSQG-126	
FT	220	AA: 23670 MW; B9A08E5E3E43F61B CRC64;	
QY	127	RRWGWKDRMGEVIGNBEDPEGVVLKDGPPMVARLVRFYPRADRVMSVLRVLYGL	186

Db 123 NAVASYKDDFELLETIPANNDTEAIRRLDRATIARRIRIVPVSNSRTVCMRVEFGCP 182 RA  
 QY 187 WRDGLLISTAPVQOTMILESEAVLNDSTYDGHVYGGLOY-GGSQLADGVGSLDDFRKSQ 245 RT  
 Db 183 FDDSLVTFNVDODD--QSGTYHDSYDGNAANSPILTGGKLGEVKNNVTNH 239 Science 282:2012-2018(1998)  
 QY 246 ELRVWPGDQYVGNSNHSFSSGGYVEMEEFDRJRAFOAMQVHVNMTL GARLPGGVCRF 305 [2]  
 Db 240 -----HKWGWRRK--RNGNVLKAFBSELNRNISGLHTSN-----EF 276 Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 PY 306 RRGPAMAVEGEPPERHNLGG-----NLGDR-----ARAVSVPLGGRARFLCRL 351 SEQUENCE FROM N.A.  
 Db 277 KKS-AKAFSSATVLFISFISDVN--RSPALGCFPPRPPWPGPPNTFSELELRGQ 405 STRAIN-BRISTOL N2;  
 RN RA  
 RT Waterston R.;  
 DR "Direct Submission";  
 QY 352 FA--GPWLFSESFISDVN-----PDSYFESTHEHDGT 382 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 Db 336 FGDSDSWFISFENPESHTNFIENLNDV-----PDSYFESTHEHDGT 382 EMBL; U41532; AA683201;  
 DR SEQUENCE 767 AA; 86900 MW; 2953C06B9416F2EE CRC64;  
 QY 406 QPVAKAEGSPTAATLGLCVALIILLLTALMWRHLRLS-----KAERVLLEELT 460 RA  
 Db 383 -----SMFAFI--FFMELIVAVILVILKRYKRVKAASSPSPNAKEL----427 RT  
 QY 461 VHLVSPGDTILINRPGPREPPOYERPRPGNPPHSPACPVPGSALLSNPARYLLATY 520 Science 282:2012-2018(1998)  
 Db 428 --LTIDNTKHH-----VSPSTYOMAR-----DNLQNALIEKMPMSPLISDY 468 [2]  
 QY 521 ARPRPGCPEPTPAWAKPTN--QAYSDYMPPEKPGAPLUPPPQNSVPHAEADVTL 577 [3]  
 Db 469 AEDPDISVCSDTA-----NTPPLYGIOPPY-QPKRNL-----SMVYKDSY-----511  
 QY 578 QGTTGGNTIYAVPALPPGAVGDPPRVDPRSRKPFKEKGQFGGEVHLCEVNDSPQDLVS 637  
 Db 512 -----GEYCT-TLP-----ELARDKLCVSRIGQEEFEDLQGEN-----548  
 QY 638 LDTPPLNVRKGHPILAVAKILRPAKTKNSAFLSLSRNDPLKEVTRIMSRKDPNIRLGLC 697  
 Db 549 -----RK-----VAKKH-----GISQDEFSPFHREIRVLSKHPNVEVVGVC 589  
 QY 698 VDOPPLCMTDYMENGDLNQFLSAHOLEDKAAGAGPQGDGAQAGPTISYPMHLVHQIA 757  
 Db 590 TICKPKLICMIMEYENGDKSY-----LKNPTQTSOCISIOMA 630  
 QY 758 SGMRYLATNFVRDLATRNCGENFTIKIADFGMRLYAGDYYVQGRAVLPIRMA 817  
 Db 631 ASGYAYLESCNFVRDILARNCLTDGESNWKIDGMARSLSQEEVYKVEKVLPIRMA 690  
 QY 818 WEGILMGKFTTASDVWARGVTLKEMVLMCRAQPFQQLDQEYVTEAEGEFFRDOGROVYL 877  
 Db 691 WEALLIGFESTASDWFGFGTYMEIFCSERPSDMDTDDYVENLOSMSMSGSLKOVLS 750  
 QY 878 RPPACPOLY-ELMLRWSREBRRPSPQSLKFL 911  
 Db 751 RPPMCPSKLYNEQICLPCUNYESSRRPSEVNHL 785  
 RESULT 5  
 Q92ZV6 PRELIMINARY; PRT; 767 AA.  
 ID Q95ZV6  
 AC Q95ZV6;  
 DT 01-DEC-2001 (Trembl. 19, Created)  
 DT 01-DEC-2001 (Trembl. 19, Last sequence update)  
 DE HYPOTHETICAL PROTEIN F11D5.3B.  
 F11D5.3  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromodorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderaeinae; Caenorhabditis;  
 OC NCBI\_TAXID=6239;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2.  
 RX MEDLINE-99069613; PubMed-9851916;  
 Q92ZV6 Query Match 20.8%; Score 1023; DB 5; Length 767;  
 Best Local Similarity 29.3%; Pred. No. 7.4e-73; Matches 266; Conservative 149; Mismatches 308; Indels 184; Gaps 31; Gaps 31;  
 Db 121 LDRAIARRIRIVPVSNSRTVCMRVEFGCPEDDSLVFVNVDODG--LQSGISYHDFS 177  
 QY 96 LVALVGTGRRHAGGLKEFSSRSYRLRSRD--RWMGKDRNQEVTSQNEDEPGVWIKD 154  
 Db 61 VITSVETQGRFDGDRGMETATAFKIQWPSLNAWASYKDDFELETIPANNDTEHARRH 120  
 QY 155 LGSPMVARYLVEYPRADRMVSYCLRVEYGLCWLWRDGLSYTAVQGQMLSEAVYLNDT 214  
 Db 121 LDRAIARRIRIVPVSNSRTVCMRVEFGCPEDDSLVFVNVDODG--LQSGISYHDFS 177  
 QY 215 YOHTVGGQY-GGLQLADGVGLDPRKQSQELRVWPGDYGVWSNHSFSSGYVEME 273  
 Db 178 YDGNLANSPLHGTGIGKLYDVGKVNNTVFNH-----HKWGWRRK--RNGNVLKAF 228  
 QY 274 FDRLRAFOAMQVHVNMTL GARLPGGVCEFRGPPAMAWEGEPMRHLGG-----N 325  
 Db 229 FSLRNISGLHTSN-----ERFKS-AKAFSSATVLFISDVN-----VSPSTYOMAR 273  
 QY 326 LGDPR-----ARAVSVPLGGRARFLCRL 418  
 Db 274 FNNPDETESEVPRWIRIYVNRKAVKIRLNGTDSWLFISEVNFSNHTNIELDD 333  
 QY 374 PAIIGGTPPPAPWMPGPPPTNNSLELPRGGQOPVAKAEGSPTAILGCLVAILLL 433  
 Db 334 VVI-----PDSVSYFSTVHDGT-----SMFAFI--FFMFLIVAVI 370  
 QY 434 IALMLWRHLRLS-----KAERVLLEELT VLSVPGDTIINRPGPREPPOYER 488  
 Db 371 ILWVLYREYRKYKASSPSPNAKEL-----LTIDNTKHH-----VSPSTYOMAR 418  
 QY 489 PRGNPPHSPACPVPGSALLSNPARYLLATYARPRPGPPNPAWAKPTN--QAYSG 545  
 Db 419 -----DNLQNALIEKMPMSPLISDYAEDPDISVCSDTA-----NTPPLYGIIDG 461  
 QY 546 DIMEPEKPGAPLUPPPQNSVPHAEADVTLQGTVGNTYAVALPGAVGDPPRVD 605  
 Db 462 PY-DTQKRNSPL-----SMVYKDSY-----E 492  
 QY 606 PSLRLKEKLGEQFGEVHLCEVSDPSQDLVSDFPLNVRKGHPILLYAVKIRDPATKA 665  
 Db 493 ARDKLCVSRIGQEEFEDLQGEN-----RK-----VAKKH-----527  
 QY 666 SFSLSRNSRNFLEKVKIMSRKDPNTIRLGLGVQDPLCMTDYMENGDLNQFLSAHOLE 725  
 Db 528 GISQADFSFHREIRVLSKHPNVEVGVCTIQKILCIMEYENGDLKSY-----581  
 QY 726 DRAEAGPQDGSQAAQGPTISYPMHLVAAQIASGMRVLALENFVRDLATRNCLVGENF 785



QY	861	ENGGEFFRQGROVLSRPPACQGGLYMLRLROWSRSEORPPFSOLRFLRADALNV	919	QY	537	-----PTWITQAVSG-----	-----DIMEPE-----	-----KPGAP	556
Db	647	QDA---IRGTGRRI-MGRPEGCQAVYVLLRWEYAADRATFKEIH----DSLNLI	696	QY	537	-----PTWITQAVSG-----	-----DIMEPE-----	-----KPGAP	556
RESULT	8	Q9BKLB	PRELIMINARY;	PRP;	1145	AA.	Q9BKLB	1145	AA.
ID	Q9BKLB	1	1	1	1	1	1	1	1
AC	Q9BKLB	1	1	1	1	1	1	1	1
DT	01-JUN-2001	(Tremblel, 17, Created)							
DT	01-JUN-2001	(Tremblel, 17, Last sequence update)							
PT	01-DEC-2001	(Tremblel, 19, Last annotation update)							
BE	ROR.								
OS	Aplysia californica (California sea hare).								
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;								
OC	Aplysiidae; Aplysia.								
OX	NCBI_TAXID=6500;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Mckay S.E., Hislop J., Scott D., Bulloch A.G., Kaczmarek L.K.,								
RA	Carew T.J., Sossin W.S.;								
RT	"Aplysia ror, a member of the TRK/MUKR family of receptor tyrosine								
RT	kinases, forms clusters on the surface of identified neuroendocrine								
RT	cells.";								
RL	Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.								
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN								
CC	TYROSINE PHOSPHATE.								
DR	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).								
DR	EMBL; AF216782; AAC23726.1; -.								
DR	HSSP; P11362; IFGK.								
DR	InterPro; IPR000719; Euk_pkinase.								
DR	InterPro; IPR00024; Fz_domain.								
DR	InterPro; IPR003599; Ig_c2.								
DR	InterPro; IPR003600; Ig_like.								
DR	InterPro; IPR003066; Ig_MHC.								
DR	InterPro; IPR00001; Kringle.								
DR	InterPro; IPR00210; Receptor_tyr_kin_II.								
DR	InterPro; IPR00249; Ser_thr_pkinase.								
DR	InterPro; IPR001245; Tyr_pkinase.								
PFam	P00047; Ig_1.								
PFam	P00069; Pinase; 1.								
PRINTS	PRINTS; PRO0018; Kringle.								
DR	SMART; SM00409; Ig_1.								
DR	SMART; SM00408; IgC2; 1.								
DR	SMART; SM00410; Ig_1_like; 1.								
DR	SMART; SM00130; KR; 1.								
DR	SMART; SM00220; S_TKc; 1.								
DR	SMART; SM0019; TyrKc; 1.								
DR	PROSITE; PS00038; FZ; 1.								
DR	PROSITE; PS00221; Kringle_1; UNKNOWN_1.								
DR	PROSITE; PS00070; Kringle_2; 1.								
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.								
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.								
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.								
DR	PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.								
KW	ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;								
KW	Receptor; Transferrase; Transmembrane; Immunoglobulin domain; Phosphorylation;								
SQ	SEQUENCE FROM N.A.	1145 AA;	125622 MW;	5C9FA652A9D1ABD	CRC64;				
DR	Query Match	13.18;	Score 648;	DB 5;	Length 1145;				
DR	Best Local Similarity	31.8%	Pred. No.	1.1e-42;					
DR	Matches	187;	Conservative	74;	Mismatches 178;	Gaps 24;			
DR	445	RILSKARRVVEEL-TVHL---SVPGDMLIN---NRPGRPB-----PPPY	484						
DR	310	RKICRDECLAELDICRETEYLMKRNHLGDLNPKCSQLOGPREGDNCIRGNMPPGS	369						
DR	485	QBRPRP---GNNPHSAPCPVNGSALLSLNSPAYRLLATYARPRP---GPSPPTPAWAK--	536						
DR	370	TSGRGKPGKGNPWNIP-----GTRRDPPRGSKGSKSKRPISDKT	410						

DR SMART; SM0082; LRRCT; 1.  
 DR SMART; SM0013; LRRNT; 1.  
 DR SMART; SM0219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS0109; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 Transmembrane; Tyrosine-protein kinase.  
 DR SEQUENCE 811 AA; 91249 MW; CE/CDICP132C1CF5 CRC64;

Query Match 12.8%; Score 633; DB 13; Length 811;  
 Best Local Similarity 44.7%; Pred. No. 1.e-41; Mismatches 80; Indels 44; Gaps 9;  
 Matches 139; Conservative 48; Mismatches 80; Indels 44; Gaps 9;  
 QY 607 RSLRKEKLGKRGCGFGEVHICE--VPSQDPLSLDFPLNVRGKPLVAKVLRDPATK 663  
 DR 524 RHNIVLKRELGEAGFKVFLAECYNYLPEQD-----KILWAVKTLK-DASD 568

QY 664 NASSLFSRNDLKEVIMSRKDPNIRLGLGVQDPLCMTDYMENGDLNQFLSHQ 723  
 DR 569 N-----RKDFHREASLTNLQHEHIVYFKYGVCEGDPPLIMFEYMRHGDLNKFRAH- 621

QY 724 LEDKAAEAGAPGDQAAQG--PTISYPMILHVAQIASGMRVATLNVRHDIAATRNCIV 780  
 DR 622 -----GPDVALMAGEGNRPALQTOSOMLHIAQOIAAGMVLAQHVFHROLATRNCIV 673

QY 781 GENFTIKTIAFDGMSRNLNYAGDYRQVGRAVLPRLRMAWECLINGKFTASDWAQGYLM 840  
 DR 674 GENLVLVKRGDFGMSRVDVSTDYRVGHTMLPRTWMPPEISYMRKFTTESDWSLGVLW 733

QY 841 EYMLICRAQPGFGQDQVIEENAGEFRDQGQVQLSRPACQGLYBLMLRCWRSSEQ 900  
 DR 734 EIFTYRK-QPWNQSLNNEVIECI----TQGR--VLRPRCPKVEVDLMLGCWQREPHM 785

QY 901 RPPFSQIHLRFL 911  
 DR 786 RLNIKEIHSLL 796

RESULT 10

ID Q9YH4 PRELIMINARY; PRT; 821 AA.  
 AC 09YH4; PRELIMINARY; PRT; 821 AA.  
 DT 01-MAY-1999 (TREMBlre. 10, Created)  
 DT 01-MAY-1999 (TREMBlre. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBlre. 19, Last annotation update)  
 DE NEUROTROPHIN RECEPTOR B XTRKB.  
 GN XTRKB.

OS Xenopus laevis (African clawed frog).  
 OC Amphibia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Xenopodinae; Xenopus.  
 OC Xenopoda; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC Xenopoda; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97101727; PubMed=8946245;  
 RA Islam N., Gagnon F., Moss T.;  
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
 mRNA are expressed in a pseudo-segmental manner within the early  
 Xenopus central nervous system.",  
 RT Int. J. Dev. Biol. 40:973-983(1996).  
 RL - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC EMBL; U39570; RADD0001.1; -  
 DR HSSP; P06213; IIRK.  
 DR InterPro; IPR00719; Euk\_pk kinase.  
 DR InterPro; IPR0359; IIG.  
 DR InterPro; IPR01611; LRR.  
 DR InterPro; IPR00483; LRR\_Cteer.  
 DR InterPro; IPR000372; LRR\_Nterm.

DR InterPro; IPR00201; Receptor\_tyr\_kin\_II.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR Pfam; PF00560; LRRCT; 1.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF0069; Pkinase; 1.  
 DR PRINTS; PRO0109; TYRKINASE.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM0013; LRRCT; 1.  
 DR SMART; SM00219; LRRNT; 1.  
 DR SMART; SM00113; LRRNT; 1.  
 DR SMART; SM0082; LRRNT; 1.  
 DR SMART; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR SMART; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 Transmembrane; Tyrosine-protein kinase.  
 DR SEQUENCE 821 AA; 92311 MW; QAB1B74F0B6FED3 CRC64;

Query Match 12.8%; Score 633; DB 13; Length 821;  
 Best Local Similarity 44.7%; Pred. No. 1.e-41; Mismatches 80; Indels 44; Gaps 9;  
 Matches 139; Conservative 48; Mismatches 80; Indels 44; Gaps 9;  
 QY 607 RSLRKEKLGKRGCGFGEVHICE--VPSQDPLSLDFPLNVRGKPLVAKVLRDPATK 663  
 DR 534 RHNIVLKRELGEAGFKVFLAECYNYLPEQD-----KILWAVKTLK-DASD 578

QY 664 NASSLFSRNDLKEVIMSRKDPNIRLGLGVQDPLCMTDYMENGDLNQFLSHQ 723  
 DR 579 N-----RKDFHREASLTNLQHEHIVYFKYGVCEGDPPLIMFEYMRHGDLNKFRAH- 631

QY 724 LEDKAAEAGAPGDQAAQG--PTISYPMILHVAQIASGMRVATLNVRHDIAATRNCIV 780  
 DR 684 GENLVLVKRGDFGMSRVDVSTDYRVGHTMLPRTWMPPEISYMRKFTTESDWSLGVLW 743

QY 781 GENFTIKTIAFDGMSRNLNYAGDYRQVGRAVLPRLRMAWECLINGKFTASDWAQGYLM 840  
 DR 841 EYMLICRAQPGFGQDQVIEENAGEFRDQGQVQLSRPACQGLYBLMLRCWRSSEQ 900  
 DR 744 EIFTYRK-QPWNQSLNNEVIECI----TQGR--VLRPRCPKVEVDLMLGCWQREPHM 795

QY 901 RPPFSQIHLRFL 911  
 DR 796 RLNIKEIHSLL 806

RESULT 11

ID Q9PSI9 PRELIMINARY; PRT; 486 AA.  
 AC Q9PSI9; PRELIMINARY; PRT; 486 AA.  
 DT 01-MAY-2000 (TREMBlre. 13, Created)  
 DT 01-DEC-2001 (TREMBlre. 13, Last sequence update)  
 DE NEUROTROPHIN RECEPTOR B XTRKB\_BETA (FRAGMENT).  
 GN XTRKB.

OS Xenopus laevis (African clawed frog).  
 OC Eutayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopoda; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopoda; Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97101727; PubMed=8946245;  
 RA Islam N., Gagnon F., Moss T.;  
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
 mRNA are expressed in a pseudo-segmental manner within the early  
 Xenopus central nervous system.",  
 RT Int. J. Dev. Biol. 40:973-983(1996).  
 RL - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR EMBL; U39672; RADD09444.1; -.

DR HSSP; P06213; LTRK.

DR InterPro; IPR007119; Euk\_pk kinase.

DR InterPro; IPR020111; Receptor\_tyr\_kin\_II.

DR InterPro; IPR01245; Tyr\_pk kinase.

DR Pfam; PF00069; pkinase\_1.

DR PRINTS; PR00109; TYRKINASE.

DR SMART; SM00219; TYRK; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50019; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.

KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;

KW Transmembrane; Tyrosine-protein kinase.

PT NON\_TER 1 1

SEQUENCE 486 AA; 54546 MW; 1645B69ABE78274FO CRC64;

Query Match 12.8%; Score 631; DB 13; Length 486;

Best Local Similarity 44.1%; Pred. No. 7.1e-42; Mismatches 80; Indels 44; Gaps 9;

Matches 137; Conservative 50; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSLRFKEKLGEGORGEVHICEVNS--PODLVSLDFPLNVRKGPHPLAVKILRDPATK 633

Db 199 RHTVILKRELGEGEGKVKVLAECNLVLEQD-----KILVAKTILK-DASD 243

QY 664 NAPSISLFSRNUFLKEVKVMSRKLKPNNPILIGVQVQDPLCMYDYMENGDLNQPLSAHQ 723

Db 244 NAA-----RKDFHREBAAELTNLHENTVKVFGVCGEGDPLIMVPEYMKHGDNLKFLRHA- 296

QY 724 LEDRAEGARGDQAGQ --PTISYPMILHVAQIASMRVIALTNVHDIAATRNLV 780

Db 297 -----GPDVAVLMAEGNLLAELTOSOMIHIQSOQIAAGMVYIASQHVTVRDIAATRNLV 348

QY 781 GENITIKIADFGMASRNLYAGDVYRQGRAVLPRMAMAWCILGKFTTASDVAWFGVILW 840

Db 349 GENILVKGDFGMSRDVYTDKVVYQGHMLPRWMPFESIMRFRFTESDWLSLGVLW 408

QY 841 EVMICRACQPFQGFLDEQVNTGEFFRQDGRYVLSRPACQGLYELMLRWSRSEQ 900

Db 409 EIFTYKG-QPWLQSNNEVTECI----TQGR--VLRPRTCPKEIYDILMLGCWOREPHM 460

QY 901 RPPSQLHRL 911

Db 461 RLNIKEIHSLL 471

RESULT 12

090599 PRELIMINARY; PRT: 790 AA.

AC Q00599; Created)

DT 01-NOV-1996 (Tremblrel\_01, last sequence update)

DT 01-NOV-1996 (Tremblrel\_01, last annotation update)

DE TROPOMYOSIN RECEPTOR KINASE.

GN CTAK.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI-TaxID=9031;

[1]

SEQUENCE FROM N.A.

Schroepel A., v Schack D., Dechant G., Barde Y.A.; "Early expression of the nerve growth factor ctk $\alpha$  in chicken sympathetic and sensory ganglia"; Mol. Cell. Neurosci. 6:0-07; -

-1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

CC HSSP; P11362; IFRK.

DR InterPro; IPR007119; Euk\_pk kinase.

DR

DR InterPro; IPR03599; IG\_MHC.

DR InterPro; IPR00306; Ig\_MHC.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR00483; LRR\_Cterm.

DR InterPro; IPR002011; Receptor\_tyr\_kin\_II.

DR InterPro; IPR001245; Tyr\_pk kinase.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF00560; LRR; 2.

DR Pfam; PF01463; LRRCT; 1.

DR Pfam; PF00069; pkinase\_1.

DR PRINTS; PR00109; TYRKINASE.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00219; TYRK; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.

KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;

KW Transmembrane; Tyrosine-protein kinase.

PT NON\_TER 1 1

SEQUENCE 575 VTQGV-----TGGNTAVPA -----LPPGAVGDP 600

Db 415 AVALLAVFASFLSMLVNLANKCGHRSKFGINRSRVALQEDDLAMSLHFMNLGSSPVSTE 474

QY 601 PRVD-----FPRSRKLFVKEKLGEGQFGEVHICEVNS--PODLVSL 638

Db 475 SKLGDGLSNFIENPQFCNACVHHVQRD-----FPRSRKLFVKEKLGEGQFGEVHICEVNS--PODLVSL 638

QY 639 DFPLNVRKGPHPLAVKILRDPATKNAESLFSRNSRNDLKEVKVMSRKLDPNTIRLLGCV 698

Db 531 -----EKTLYAVKAK-ETESA-----RLDFRREAEELVQHEHTVFKYGVCT 574

QY 699 QDPPLCMYDYMENGDLNQPLSAHQDEADGKAAEGPQGQQAQOPTISYPMILHVARQAS 758

Db 575 EGEPLIMVFEYMKHGDNLNFRSHGPDAAKTD--QGQGQPCGQTLSH--MLOIATQIAS 630

QY 759 GMYLATUNFVHDLATINCLVGENFNTIKIADEGMSRNLLIAGDVYRQGRAVLPRIMW 818

Db 631 GMVYLAASHIFVHDLATRNLVCLVHDLVKGIGPMGMSRDIYSDYUFGRTMLPIMRNP 690

QY 819 ECLIMGKETTASDQWAFQTLWVMLCRAQPGQQLTDEQVNTENAGERFRDQGRQVYLW 878

Db 691 ESTLYRKFTESDIWSQVWLFYTKG-QPWLQSNTEAECI----TQGR--LER 742

QY 879 PPACQPGQVYELMLRCWSRESEORPPFSQH 908

Db 743 PRTPCSEVFDIMOSCWOREPOOROIDH 772

RESULT 13

Q27656 PRELIMINARY; PRT; 699 AA.  
 ID Q27656; AC 027656; DT 01-NOV-1996 (TREMBrel. 01, Created)  
 DT 01-NOV-1996 (TREMBrel. 19, Last annotation update)  
 DE SPONGE RECEPTOR TYROSINE KINASE (EC 2.7.1.112).  
 OS Geodia cydonium (Sponge).  
 OC Buka-yota; Metz-za; Porifera; Demospongiae; Tetractinomorpha;  
 Astrophorida; Geodidae; Geodia.  
 NCBI\_TAXID=6047;  
 RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE=95142935; PubMed=7840899;  
 RA Gamulin V., Rinkevich B., Schaecke H., Kruse M., Mueller I.M.,  
 Werner E.G.;  
 RT "Cell adhesion receptors and nuclear receptors are highly conserved  
 RT from the lowest metazoa (marine sponges) to vertebrates";  
 RL Biol. Chem. Hoppe-Seyler 375:583-588(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95251882; PubMed=7734153;  
 RA Schaecke H., Rinkevich B., Gamulin V., Mueller I.M., Mueller W.E.G.;  
 RT "Immunoglobulin-like domain is present in the extracellular part of  
 receptor tyrosine kinase gene from the sponge Geodia cydonium";  
 RL J. Mol. Recognit. 7:273-276(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97224609; PubMed=9060390;  
 RA Gamulin V., Skorokhod A., Mueller M., Schaecke H., Mueller W.E.G.;  
 RT "Experimental indication in favor of the introns-late theory: The  
 receptor tyrosine kinase gene from the sponge Geodia cydonium";  
 RL J. Mol. Evol. 44:242-252(1997).  
 CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL: X77528; CAA56631; -. HSSP: P0631; IAD5; InterPro: IPR00719; Euk\_pk kinase.  
 DR InterPro: IPR003599; Ig; DR InterPro: IPR003600; Ig\_like.  
 DR InterPro: IPR003065; Ig\_MHC.  
 DR InterPro: IPR001245; Tyr\_pk kinase.  
 DR Pfam: PF00047; Ig; DR SMART: SM00409; Ig; DR SMART: SM00410; Ig\_like; DR SMART: SM00219; TyrK; PROSITE: PS50011; PROTEIN\_KINASE\_DOMAIN; PROSITE: PS00019; PROTEIN\_KINASE\_TYR; DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; KW Transferease; Transmembrane; Tyrosine-protein kinase. SEQUENCE 699 AA; MW: 804825AA0851CCE CRC64;

QY 544 SGDMEPKGAPLLPPPPQNSVPHAEADIVTLQ-GVTGGNT-YAVPALD----- 592  
 ID 075682 PRELIMINARY; PRT; 839 AA.  
 AC 075682; DT 01-NOV-1998 (TREMBrel. 08, Created)  
 DT 01-NOV-1998 (TREMBrel. 19, Last annotation update)  
 DE TRKC PROTEIN.  
 GN TRKC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metz-za; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI\_TAXID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE=9849483; PubMed=9778053;  
 RA Ichaso N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.; RT "Genomic characterization of the human trkC gene.";  
 CC CC  
 RL Oncogene 17:1871-1875(1998).  
 DR -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL: AJ224521; CAA12029; 1; DR EMBL: AJ224522; CAA12029; 1; JOINED.  
 DR EMBL: AJ224523; CAA12029; 1; JOINED.  
 DR EMBL: AJ224524; CAA12029; 1; JOINED.  
 DR EMBL: AJ224525; CAA12029; 1; JOINED.  
 DR EMBL: AJ224526; CAA12029; 1; JOINED.  
 DR EMBL: AJ224527; CAA12029; 1; JOINED.  
 DR EMBL: AJ224528; CAA12029; 1; JOINED.  
 DR EMBL: AJ224529; CAA12029; 1; JOINED.  
 DR EMBL: AJ224530; CAA12029; 1; JOINED.  
 DR EMBL: AJ224531; CAA12029; 1; JOINED.  
 DR EMBL: AJ224532; CAA12029; 1; JOINED.  
 DR EMBL: AJ224533; CAA12029; 1; JOINED.  
 DR EMBL: AJ224534; CAA12029; 1; JOINED.  
 DR EMBL: AJ224535; CAA12029; 1; JOINED.  
 DR HSSP: P06213; 1TRK.  
 DR InterPro: IPR00719; Euk\_pk kinase.

Query Match: 12.7%; Score 623; 5; DB 5; Length 699;  
 Best Local Similarity 31.6%; Pred. No. 4.8e-41;  
 Matches 195; Conservative 83; Mismatches 176; Indels 163; Gaps 26;

QY 409 AKKEGSPTRALIGVAVIILLILLI-MLWPLHWRLLSKAERRVVEELTHLS- 464  
 ID 136 SNSGGSNSNVEVAGLITLILALIILIFVWVYCYR----RGKIDGSCRELSCG 189  
 DR 465 ---VPGDTILINRPGPPEPPYQEPRPRGNNPPHSAPCVPNGSALLS----- 509  
 DR 190 SCSCVp---LLAALKGKWLPRHRENLDK-----NGTFLRLNERNHADNT 234  
 QY 510 --NFAVRLLATYARPRPGRGP-----TPAWAKPT--NT--QY 543  
 DR 235 IYSVWQPKLKKISKSPP--PLPPLLTETELNEUTSIDEKEELSPQEKPRTRNGLSTY 292

DR InterPro; IPR003599; Ig\_MHC.  
 DR InterPro; IPR03006; Ig\_MHC.  
 DR InterPro; IPR01611; LRR.  
 DR InterPro; IPR00483; LRR\_Cterm.  
 DR InterPro; IPR00372; LRR\_Nterm.  
 DR InterPro; IPR02011; Receptor\_tyr\_kin\_II.  
 DR InterPro; IPR01245; Tyr\_Pkinase.  
 PFam; PF00047; Ig; 1.  
 DR PFam; PF00580; LRR; 2.  
 PFam; PF01463; LRRCT; 1.  
 PFam; PF01462; LRRNT; 1.  
 PFam; PF00659; kinase; 1.  
 SMART; SM00409; Ig; 1.  
 SMART; SM00882; LRRCT; 1.  
 SMART; SM00013; LRRNT; 1.  
 SMART; SM00219; TYRK; 1.  
 PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 KW transmembrane; Tyrosine-protein kinase.  
 SEQUENCE: 839 AA; 9428 MW; 7FEE8846830083C08 C064;  
 SQ

RESULT	15	QY	904	FSOLH	908
Q15655		Db	481	IKDVH	485
ID	Q15655				
	PRELIMINARY;	PRT;	503	AA.	

Mon Oct 7 15:50:49 2002

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Search completed: October 4, 2002, 07:45:30  
Job time: 285 sec